

cells with PE-labeled goat anti-human Ig to detect chimeric SDF-Fc polypeptide remaining after the 3- or 15-hour incubation (data not shown).

Down-regulation of receptor by binding of MIP-1 α -Fc and MIP-1 β -Fc chimeric polypeptides to cells is determined by an assay for receptor down-regulation analogous to that described above.

SEQUENCE LISTING

- 10 (1) GENERAL INFORMATION:
- (i) APPLICANT: Herrmann, Steve
Swanberg, Stephen
- 15 (ii) TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING
CHEMOKINE DOMAINS
- (iii) NUMBER OF SEQUENCES: 10
- 20 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genetics Insititute, Inc.
(B) STREET: 87 CambridgePark
(C) CITY: Cambridge
(D) STATE: MA
25 (E) COUNTRY: USA
(F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
30 (B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
35 (A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: Sprunger, Suzanne
(B) REGISTRATION NUMBER: P-41,323
(C) REFERENCE/DOCKET NUMBER: GI5291
- (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: (617) 498-8284
(B) TELEFAX: (617) 876-5851
- (2) INFORMATION FOR SEQ ID NO:1:
- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 328 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

1	Met	Asn	Ala	Lys	Val	Val	Val	Val	Leu	Val	Leu	Val	Leu	Thr	Ala	Leu
					5				10						15	
15	Cys	Leu	Ser	Asp	Gly	Lys	Pro	Val	Ser	Leu	Ser	Tyr	Arg	Cys	Pro	Cys
				20					25					30		
	Arg	Phe	Phe	Glu	Ser	His	Val	Ala	Arg	Ala	Asn	Val	Lys	His	Leu	Lys
			35					40					45			
20	Ile	Leu	Asn	Thr	Pro	Asn	Cys	Ala	Leu	Gln	Ile	Val	Ala	Arg	Leu	Lys
		50					55					60				
	Asn	Asn	Asn	Arg	Gln	Val	Cys	Ile	Asp	Pro	Lys	Leu	Lys	Trp	Ile	Gln
25						70					75					80
	Glu	Tyr	Leu	Glu	Lys	Ala	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Gly	Ser	Gly
					85					90					95	
30	Ser	Gly	Ser	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Ser	Cys	Pro	Ala
				100					105					110		
	Pro	Glu	Phe	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
			115					120					125			
35	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
		130					135					140				
	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val
40		145				150					155					160
	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
				165					170					175		
45	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
			180					185						190		
	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly
		195					200						205			
50	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
		210					215					220				
	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr
55		225				230					235					240
	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
				245					250					255		
60	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
			260						265					270		
	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr

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Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe
290 295 300

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
305 310 315 320

Ser Leu Ser Leu Ser Leu Gly Lys
325

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1222 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCGGCCGCGC CATGAACGCC AAGGTCGTGG TCGTGCTGGT CCTCGTGCTG ACCGCGCTCT 60
GCCTCAGCGA CGGGAAGCCC GTCAGCCTGA GCTACAGATG CCCATGCCGA TTCTTCGAAA 120
GCCATGTTGC CAGAGCCAAC GTCAAGCATC TCAAAATTCT CAACACTCCA AACTGTGCCC 180
TTCAGATTGT AGCCCGGCTG AAGAACAACA ACAGACAAGT GTGCATTGAC CCGAAGCTAA 240
AGTGATTCA GGAGTACCTG GAGAAAGCTT TAAACAAGGG ATCCGGCTCT GGGAGCGGCT 300
CTGGCTCTGA GTCCAAATAT GGTCCCCCAT GCCCATCATG TCCAGGTAAG CCAACCCAGG 360
CCTCGCCCTC CAGCTCAAGG CGGGACAGGT GCCCTAGAGT AGCCTGCATC CAGGGACAGG 420
CCCCAGCCGG GTGCTGACGC ATCCACCTCC ATCTCTTCCT CAGCACCTGA GTTCGAGGGG 480
GCACCATCAG TCTTCCTGTT CCCCCAAAA CCAAGGACA CTCTCATGAT CTCCCGGACC 540
CCTGAGGTCA CGTGCGTGGT GGTGGACGTG AGCCAGGAAG ACCCCGAGGT CCAGTTCAAC 600
TGGTACGTGG ATGGCGTGGA GGTGCATAAT GCCAAGACAA AGCCGCGGGA GGAGCAGTTC 660
AACAGCACGT ACCGTGTGGT CAGCGTCCTC ACCGTCCTGC ACCAGGACTG GCTGAACGGC 720
AAGGAGTACA AGTGCAAGGT CTCCAACAAA GGCTCCCCGT CCTCCATCGA GAAAACCATC 780
TCCAAAGCCA AAGGTGGGAC CCACGGGGTG CGAGGGCCAC ACGGACAGAG GTCAGCTCGG 840
CCCACCCTCT GCCCTGGGAG TGACCGCTGT GCCAACCTCT GTCCCTACAG GGCAGCCCCG 900
AGAGCCACAG GTGTACACCC TGCCCCCATC CCAGGAGGAG ATGACCAAGA ACCAGGTCAG 960
CCTGACCTGC CTGGTCAAAG GCTTCTACCC CAGCGACATC GCCGTGGAGT GGGAGAGCAA 1020
TGGGCAGCCG GAGAACAAC AAGAGACCAC GCCTCCCGTG CTGGACTCCG ACGGCTCCTT 1080
CTTCCTCTAC AGCAGGCTAA CCGTGGACAA GAGCAGGTGG CAGGAGGGGA ATGTCTTCTC 1140

ATGCTCCGTG ATGCATGAGG CTCTGCACAA CCACTACACA CAGAAGAGCC TCTCCCTGTC 1200
 TCTGGGTAAA TGATAAGAAT TC 1222

5 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 326 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

20	Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu	1 5 10 15
25	Cys Leu Ser Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe	20 25 30
30	Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu	35 40 45
35	Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn	50 55 60
40	Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr	65 70 75 80
45	Leu Glu Lys Ala Leu Asn Lys Gly Ser Gly Ser Gly Ser Gly Ser Gly	85 90 95
50	Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu	100 105 110
55	Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp	115 120 125
60	Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp	130 135 140
	Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly	145 150 155 160
	Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn	165 170 175
	Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp	180 185 190
	Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro	195 200 205
	Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu	210 215 220
	Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn	225 230 235 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 245 250 255
 5 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 260 265 270
 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
 275 280 285
 10 Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
 290 295 300
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 305 310 315 320
 15 Ser Leu Ser Leu Gly Lys
 325

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCGGCCGCGC CATGAACGCC AAGGTCGTGG TCGTGCTGGT CCTCGTGCTG ACCGCGCTCT 60
 35 GCCTCAGCAA GCCCGTCAGC CTGAGCTACA GATGCCCATG CCGATTCTTC GAAAGCCATG 120
 TTGCCAGAGC CAACGTCAAG CATCTCAAAA TTCTCAACAC TCCAAACTGT GCCCTTCAGA 180
 40 TTGTAGCCCG GCTGAAGAAC AACACAGAC AAGTGTGCAT TGACCCGAAG CTAAAGTGGA 240
 TTCAGGAGTA CCTGGAGAAA GCTTTAAACA AGGGATCCGG CTCTGGGAGC GGCTCTGGCT 300
 CTGAGTCCAA ATATGGTCCC CCATGCCCAT CATGTCCAGG TAAGCCAACC CAGGCCTCGC 360
 45 CCTCCAGCTC AAGGCGGGAC AGGTGCCCTA GAGTAGCCTG CATCCAGGGA CAGGCCCCAG 420
 CCGGGTGCTG ACGCATCCAC CTCCATCTCT TCCTCAGCAC CTGAGTTCGA GGGGGCACCA 480
 50 TCAGTCTTCC TGTTCCCCC AAAACCCAAG GACACTCTCA TGATCTCCCG GACCCCTGAG 540
 GTCACGTGCG TGGTGGTGGA CGTGAGCCAG GAAGACCCCG AGGTCCAGTT CAACTGGTAC 600
 GTGGATGGCG TGGAGGTGCA TAATGCCAAG ACAAGCCGC GGGAGGAGCA GTTCAACAGC 660
 55 ACGTACCGTG TGGTCAGCGT CCTCACCCTC CTGCACCAGG ACTGGCTGAA CGGCAAGGAG 720
 TACAAGTGCA AGGTCTCCAA CAAAGGCCTC CCGTCTCCA TCGAGAAAAC CATCTCCAAA 780
 60 GCCAAAGGTG GGACCCACGG GGTGCGAGGG CCACACGGAC AGAGGTCAGC TCGGCCCCACC 840
 CTCTGCCCTG GGAGTGACCG CTGTGCCAAC CTCTGTCCCT ACAGGGCAGC CCCGAGAGCC 900

ACAGGTGTAC ACCCTGCCCC CATCCCAGGA GGAGATGACC AAGAACCAGG TCAGCCTGAC 960
 CTGCCTGGTC AAAGGCTTCT ACCCCAGCGA CATCGCCGTG GAGTGGGAGA GCAATGGGCA 1020
 5 GCCGAGAAAC AACTACAAGA CCACGCCTCC CGTGCTGGAC TCCGACGGCT CCTTCTTCCT 1080
 CTACAGCAGG CTAACCGTGG ACAAGAGCAG GTGGCAGGAG GGAATGTCT TCTCATGCTC 1140
 10 CGTGATGCAT GAGGCTCTGC ACAACCACTA CACACAGAAG AGCCTCTCCC TGTCTCTGGG 1200
 TAAATGATAA GAATTC 1216

(2) INFORMATION FOR SEQ ID NO:5:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala
 1 5 10 15
 30 Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala
 20 25 30
 35 Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala
 35 40 45
 Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe
 50 55 60
 40 Leu Thr Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp
 65 70 75 80
 Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala Gly Ser Gly Ser
 85 90 95
 45 Gly Ser Gly Ser Gly Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser
 100 105 110
 50 Cys Pro Ala Pro Glu Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro
 115 120 125
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 130 135 140
 55 Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
 145 150 155 160
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 165 170 175
 60 Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 180 185 190

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 195 200 205
 5 Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
 210 215 220
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
 225 230 235 240
 10 Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 245 250 255
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 260 265 270
 15 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 275 280 285
 Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
 290 295 300
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 305 310 315 320
 25 Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 325 330

(2) INFORMATION FOR SEQ ID NO:6:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCGGCCGCCC AATCATGCAG GTCTCCACTG CTGCCCTTGC TGTCTCCTC TGCACCATGG 60
 45 CTCTCTGCAA CCAGTTCTCT GCATCAC TTG CTGCTGACAC GCCGACCGCC TGCTGCTTCA 120
 GCTACACCTC CCGGCAGATT CCACAGAATT TCATAGCTGA CTACTTTGAG ACGAGCAGCC 180
 AGTGCTCCAA GCCCGGTGTC ATCTTCCTAA CCAAGCGAAG CCGGCAGGTC TGTGCTGACC 240
 50 CCAGTGAGGA GTGGGTCCAG AAATACGTCA GTGACCTGGA GCTGAGTGCC GGATCCGGCT 300
 CTGGGAGCGG CTCTGGCTCT GAGTCCAAAT ATGGTCCCCC ATGCCCATCA TGTCCAGGTA 360
 55 AGCCAACCCA GGCCTCGCCC TCCAGCTCAA GGCGGGACAG GTGCCCTAGA GTAGCCTGCA 420
 TCCAGGGACA GGCCCCAGCC GGGTGCTGAC GCATCCACCT CCATCTCTTC CTCAGCACCT 480
 GAGTTCGAGG GGGCACCATC AGTCTTCCTG TTCCCCC CAA AACCCAAGGA CACTCTCATG 540
 60 ATCTCCCGGA CCCCTGAGGT CACGTGCGTG GTGGTGACG TGAGCCAGGA AGACCCCGAG 600
 GTCCAGTTCA ACTGGTACGT GGATGGCGTG GAGGTGCATA ATGCCAAGAC AAAGCCGCGG 660

GAGGAGCAGT TCAACAGCAC GTACCGTGTG GTCAGCGTCC TCACCGTCCT GCACCAGGAC 720
 TGGCTGAACG GCAAGGAGTA CAAGTGCAAG GTCTCCAACA AAGGCCTCCC GTCCTCCATC 780
 5 GAGAAAACCA TCTCCAAAGC CAAAGGTGGG ACCCACGGGG TGCAGGGGCC ACACGGACAG 840
 AGGTCAGCTC GGCCACCCCT CTGCCCTGGG AGTGACCGCT GTGCCAACCT CTGTCCCTAC 900
 10 AGGGCAGCCC CGAGAGCCAC AGGTGTACAC CCTGCCCCCA TCCCAGGAGG AGATGACCAA 960
 GAACCAGGTC AGCCTGACCT GCCTGGTCAA AGGCTTCTAC CCCAGCGACA TCGCCGTGGA 1020
 GTGGGAGAGC AATGGGCAGC CGGAGAACAA CTACAAGACC ACGCCTCCCG TGCTGGACTC 1080
 15 CGACGGCTCC TTCTTCCTCT ACAGCAGGCT AACCGTGGAC AAGAGCAGGT GGCAGGAGGG 1140
 GAATGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC AACCACTACA CACAGAAGAG 1200
 CCTCTCCCTG TCTCTGGGTA AATGATAAGA ATTC 1234

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Lys Leu Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala
 1 5 10 15
 Phe Cys Ser Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr
 20 25 30
 Ala Cys Cys Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val
 35 40 45
 Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val
 50 55 60
 Phe Gln Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser
 65 70 75 80
 Trp Val Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn Gly Ser Gly Ser
 85 90 95
 Gly Ser Gly Ser Gly Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser
 100 105 110
 Cys Pro Ala Pro Glu Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro
 115 120 125
 60 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 130 135 140
 Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn

	145		150		155		160
5	Trp Tyr Val Asp	Gly Val Glu Val His	Asn Ala Lys Thr Lys Pro Arg				
		165	170	175			
	Glu Glu Gln Phe Asn Ser Thr Tyr Arg	Val Val Ser Val Leu Thr Val					
		180	185	190			
10	Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser						
		195	200	205			
	Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys						
		210	215	220			
15	Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu						
		225	230	235			240
	Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe						
		245	250	255			
20	Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu						
		260	265	270			
	Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe						
25		275	280	285			
	Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly						
		290	295	300			
30	Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr						
		305	310	315			320
	Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys						
		325	330				

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

50	GCGGCCGCCA ATACCATGAA GCTCTGCGTG ACTGTCTGT CTCTCCTCAT GCTAGTAGCT	60
	GCCTTCTGCT CTCCAGCGCT CTCAGCACCA ATGGGCTCAG ACCCTCCCAC CGCCTGCTGC	120
55	TTTTCTTACA CCGCGAGGAA GCTTCCTCGC AACTTTGTGG TAGATTACTA TGAGACCAGC	180
	AGCCTCTGCT CCCAGCCAGC TGTGGTATTC CAAACCAAAA GAAGCAAGCA AGTCTGTGCT	240
	GATCCCACTG AATCCTGGGT CCAGGAGTAC GTGTATGACC TGGAACTGAA CGGATCCGGC	300
60	TCTGGGAGCG GCTCTGGCTC TGAGTCCAAA TATGGTCCCC CATGCCCATC ATGTCCAGGT	360
	AAGCCAACCC AGGCCTCGCC CTCCAGCTCA AGGCGGGACA GGTGCCCTAG AGTAGCCTGC	420

ATCCAGGGAC AGGCCCCAGC CGGGTGCTGA CGCATCCACC TCCATCTCTT CCTCAGCACC 480
 TGAGTTCGAG GGGGCACCAT CAGTCTTCCT GTTCCCCCA AAACCCAAGG AACTCTCAT 540
 5 GATCTCCCGG ACCCCTGAGG TCACGTGCGT GGTGGTGGAC GTGAGCCAGG AAGACCCGA 600
 GGTCCAGTTC AACTGGTACG TGGATGGCGT GGAGGTGCAT AATGCCAAGA CAAAGCCGCG 660
 10 GGAGGAGCAG TTCAACAGCA CGTACCGTGT GGTACGCGTC CTCACCGTCC TGCACCAGGA 720
 CTGGCTGAAC GGCAAGGAGT ACAAGTGCAA GGTCTCCAAC AAAGGCCTCC CGTCCTCCAT 780
 CGAGAAAACC ATCTCCAAAG CCAAAGGTGG GACCCACGGG GTGCGAGGGC CACACGGACA 840
 15 GAGGTCAGCT CGGCCACCC TCTGCCCTGG GAGTGACCGC TGTGCCAACC TCTGTCCCTA 900
 CAGGGCAGCC CCGAGAGCCA CAGGTGTACA CCCTGCCCC ATCCAGGAG GAGATGACCA 960
 AGAACCAGGT CAGCCTGACC TGCCTGGTCA AAGGCTTCTA CCCCAGCGAC ATCGCCGTGG 1020
 20 AGTGGGAGAG CAATGGGCAG CCGGAGAACA ACTACAAGAC CACGCCTCCC GTGCTGGACT 1080
 CCGACGGCTC CTTCTTCCTC TACAGCAGGC TAACCGTGA CAAGAGCAGG TGGCAGGAGG 1140
 25 GGAATGTCTT CTCATGCTCC GTGATGCATG AGGCTCTGCA CAACCACTAC ACACAGAAGA 1200
 GCCTCTCCCT GTCTCTGGGT AAATGATAAG AATTC 1235

(2) INFORMATION FOR SEQ ID NO:9:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 92 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

45 Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala
 1 5 10 15
 Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala
 20 25 30
 50 Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala
 35 40 45
 Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe
 50 55 60
 55 Leu Thr Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp
 65 70 75 80
 60 Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala
 85 90

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 92 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: protein

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

15

Met Lys Leu Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala
 1 5 10 15

Phe Cys Ser Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr
 20 25 30

20

Ala Cys Cys Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val
 35 40 45

25

Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val
 50 55 60

Phe Gln Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser
 65 70 75 80

30

Trp Val Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn
 85 90